RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: _09/466,778A_

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Revised 04/24/2003

1600

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                RAW SEQUENCE LISTING              DATE: 08/14/2003
                PATENT APPLICATION:  US/09/466,778A    TIME: 15:07:38

                Input Set : A:\PF487 subst. SL Aug2003.txt
                Output Set: N:\CRF4\08142003\I466778A.raw

 3 <110> APPLICANT: Hastings, et al.
 5 <120> TITLE OF INVENTION: Novel Hyaluronan-Binding Proteins and Encoding Genes
 7 <130> FILE REFERENCE: PF487
 9 <140> CURRENT APPLICATION NUMBER: 09/466,778A
10 <141> CURRENT FILING DATE: 1999-12-20
12 <150> PRIOR APPLICATION NUMBER: 60/113,871
13 <151> PRIOR FILING DATE: 1998-12-23
15 <160> NUMBER OF SEQ ID NOS: 37
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 6761
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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25 <221> NAME/KEY: CDS
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28 <220> FEATURE:
29 <221> NAME/KEY: misc_feature
30 <222> LOCATION: (6342)
31 <223> OTHER INFORMATION: n equals a, t, g or c
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40 <222> LOCATION: (6529)
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44 <221> NAME/KEY: misc_feature
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49 <221> NAME/KEY: misc_feature
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51 <223> OTHER INFORMATION: n equals a, t, g or c
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55 <222> LOCATION: (6688)
56 <223> OTHER INFORMATION: n equals a, t, g or c
58 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
60 <222> LOCATION: (6724)
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Does Not Comply
Corrected Diskette Needed

pp 2, 6-7

RAW SEQUENCE LISTING   DATE: 08/14/2003
PATENT APPLICATION: US/09/466,778A   TIME: 15:07:38

Input Set : A:\PF487 subst. SL Aug2003.txt
Output Set: N:\CRF4\08142003\I466778A.raw

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69 <221> NAME/KEY: misc_feature
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71 <223> OTHER INFORMATION: n equals a, t, g or c
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74 <221> NAME/KEY: misc_feature
75 <222> LOCATION: (6753)
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83 ggccacgcag acaggccggg tgttcctgca gctgagggtc gccgtggcc atg atg gac 178
84                                                        Met Met Asp
85                                                          1
87 cag ggc tgc cgg gaa atc ctt acc aca gcg ggc cct ttc acc gtg ctg  226
88 Gln Gly Cys Arg Glu Ile Leu Thr Thr Ala Gly Pro Phe Thr Val Leu
89       5               10              15
91 gtg cca tcc gtc tcc tcc ttc tcc tcc agg acc atg aat gca tcc ctt  274
92 Val Pro Ser Val Ser Ser Phe Ser Ser Arg Thr Met Asn Ala Ser Leu
93 20              25              30                      35
95 gcc cag cag ctc tgt aga cag cac atc atc gca ggg cag cac atc ctg  322
96 Ala Gln Gln Leu Cys Arg Gln His Ile Ile Ala Gly Gln His Ile Leu
97               40              45                      50
99 gag gac aca agg acc caa caa aca cga agg tgg tgg acg ctg gcc ggg  370
100 Glu Asp Thr Arg Thr Gln Gln Thr Arg Arg Trp Trp Thr Leu Ala Gly
101             55              60                      65
103 cag gag atc acc gtc acc ttt aac caa ttc acg aaa tac tcc tac aag  418
104 Gln Glu Ile Thr Val Thr Phe Asn Gln Phe Thr Lys Tyr Ser Tyr Lys
105             70              75              80
107 tac aaa gac cag ccc cag cag acg ttc aac atc tac aag gcc aac aac  466
108 Tyr Lys Asp Gln Pro Gln Gln Thr Phe Asn Ile Tyr Lys Ala Asn Asn
109       85              90              95
111 ata gca gct aat ggc gtc ttc cac gtg gtc act ggc ctg cgg tgg cag  514
112 Ile Ala Ala Asn Gly Val Phe His Val Val Thr Gly Leu Arg Trp Gln
113 100             105             110                     115
115 gcc ccc tct ggg acc cct ggg gat ccc aag aga act atc gga cag atc  562
116 Ala Pro Ser Gly Thr Pro Gly Asp Pro Lys Arg Thr Ile Gly Gln Ile
117             120             125             130
119 ctc gcc tct acc gag gcc ttc agc cgc ttt gaa acc atc ctg gag aac  610
120 Leu Ala Ser Thr Glu Ala Phe Ser Arg Phe Glu Thr Ile Leu Glu Asn
121             135             140             145
123 tgt ggg ctg ccc tcc atc ctg gac gga cct ggg ccc ttc aca gtc ttt  658
124 Cys Gly Leu Pro Ser Ile Leu Asp Gly Pro Gly Pro Phe Thr Val Phe
125       150             155             160
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what about "n" at location 6749?

(see p.6)

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127 gcc cca agc aat gag gct gtg gac agc ttg cgt gac ggc cgc ctg atc    706
128 Ala Pro Ser Asn Glu Ala Val Asp Ser Leu Arg Asp Gly Arg Leu Ile
129     165             170             175
131 tac ctc ttc aca gcg ggt ctc tct aaa ctg cag gag ttg gtg cgg tac    754
132 Tyr Leu Phe Thr Ala Gly Leu Ser Lys Leu Gln Glu Leu Val Arg Tyr
133 180             185             190             195
135 cac atc tac aac cac ggc cag ctg acc gtt gag aag ctc atc tcc aag    802
136 His Ile Tyr Asn His Gly Gln Leu Thr Val Glu Lys Leu Ile Ser Lys
137             200             205             210
139 ggt cgg atc ctc acc atg gcg aac cag gtc ctg gct gtg aac att tct    850
140 Gly Arg Ile Leu Thr Met Ala Asn Gln Val Leu Ala Val Asn Ile Ser
141             215             220             225
143 gag gag ggg cgc atc ctg ctg gga ccc gag ggg gtc ccg ctg cag agg    898
144 Glu Glu Gly Arg Ile Leu Leu Gly Pro Glu Gly Val Pro Leu Gln Arg
145         230             235             240
147 gta gac gtg atg gcc gcc aat ggc gtg atc cac atg ctg gac ggc atc    946
148 Val Asp Val Met Ala Ala Asn Gly Val Ile His Met Leu Asp Gly Ile
149     245             250             255
151 ctg ctg ccc ccg acc atc ctg ccc atc ctg ccc aag cac tgc agc gag    994
152 Leu Leu Pro Pro Thr Ile Leu Pro Ile Leu Pro Lys His Cys Ser Glu
153 260             265             270             275
155 gag cag cac aag att gtg gcg ggc tcc tgt gtg gac tgc caa gcc ctg    1042
156 Glu Gln His Lys Ile Val Ala Gly Ser Cys Val Asp Cys Gln Ala Leu
157             280             285             290
159 aac acc agc acg tgt ccc ccc aac agt gtg aag ctg gac atc ttc ccc    1090
160 Asn Thr Ser Thr Cys Pro Pro Asn Ser Val Lys Leu Asp Ile Phe Pro
161             295             300             305
163 aag gag tgt gtc tac atc cat gac cca acg ggg ctc aat gtg cta aag    1138
164 Lys Glu Cys Val Tyr Ile His Asp Pro Thr Gly Leu Asn Val Leu Lys
165         310             315             320
167 aag ggc tgt gcc agc tac tgc aac caa acc atc atg gaa caa ggc tgc    1186
168 Lys Gly Cys Ala Ser Tyr Cys Asn Gln Thr Ile Met Glu Gln Gly Cys
169     325             330             335
171 tgc aaa ggt ttt ttc ggg cct gac tgc acg cag tgt cct ggg ggc ttc    1234
172 Cys Lys Gly Phe Phe Gly Pro Asp Cys Thr Gln Cys Pro Gly Gly Phe
173 340             345             350             355
175 tcc aac ccc tgc tat ggc aaa ggc aat tgc agt gat ggg atc cag ggc    1282
176 Ser Asn Pro Cys Tyr Gly Lys Gly Asn Cys Ser Asp Gly Ile Gln Gly
177             360             365             370
179 aat ggg gcc tgc ctc tgc ttc cca gac tac aag ggc atc gcc tgc cac    1330
180 Asn Gly Ala Cys Leu Cys Phe Pro Asp Tyr Lys Gly Ile Ala Cys His
181             375             380             385
183 atc tgc tcg aac cca aac aag cat gga gag caa tgc cag gaa gac tgc    1378
184 Ile Cys Ser Asn Pro Asn Lys His Gly Glu Gln Cys Gln Glu Asp Cys
185             390             395             400
187 ggc tgt gtc cat ggt ctc tgc gac aac cgc cca ggc agt ggg ggg gtg    1426
188 Gly Cys Val His Gly Leu Cys Asp Asn Arg Pro Gly Ser Gly Gly Val
189     405             410             415
191 tgc cag cag ggc acg tgt gcc cct ggc ttc agt ggc cgg ttc tgc aac    1474
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192 Cys Gln Gln Gly Thr Cys Ala Pro Gly Phe Ser Gly Arg Phe Cys Asn
193 420               425               430               435
195 gag tcc atg ggg gac tgt ggg ccc aca ggg ctg gcc cag cac tgc cac    1522
196 Glu Ser Met Gly Asp Cys Gly Pro Thr Gly Leu Ala Gln His Cys His
197               440               445               450
199 ctg cat gcc cgc tgt gtt agc cag gag ggt gtt gcc aga tgt cgc tgt    1570
200 Leu His Ala Arg Cys Val Ser Gln Glu Gly Val Ala Arg Cys Arg Cys
201               455               460               465
203 ctt gat ggc ttt gag ggt gat ggc ttc tcc tgc aca cct agc aac ccc    1618
204 Leu Asp Gly Phe Glu Gly Asp Gly Phe Ser Cys Thr Pro Ser Asn Pro
205               470               475               480
207 tgc tcc cac ccg gac cgt gga ggc tgc tca gag aat gct gag tgt gtc    1666
208 Cys Ser His Pro Asp Arg Gly Gly Cys Ser Glu Asn Ala Glu Cys Val
209     485               490               495
211 cct ggg tcc ctg ggc acc cac cac tgc aca tgc cac aaa ggc tgg agt    1714
212 Pro Gly Ser Leu Gly Thr His His Cys Thr Cys His Lys Gly Trp Ser
213 500               505               510               515
215 ggg gat ggc cgc gtc tgt gtg gct att gac gag tgt gag ctg gac gtg    1762
216 Gly Asp Gly Arg Val Cys Val Ala Ile Asp Glu Cys Glu Leu Asp Val
217               520               525               530
219 aga ggt ggc tgc cac acc gat gcc ctc tgc agc tat gtg ggc ccc ggg    1810
220 Arg Gly Gly Cys His Thr Asp Ala Leu Cys Ser Tyr Val Gly Pro Gly
221               535               540               545
223 cag agc cga tgc acc tgc aag ctg ggc ttt gcc ggg gat ggc tac cag    1858
224 Gln Ser Arg Cys Thr Cys Lys Leu Gly Phe Ala Gly Asp Gly Tyr Gln
225         550               555               560
227 tgc agc ccc atc gac ccc tgc cgg gca ggc aat ggc ggc tgc cac ggc    1906
228 Cys Ser Pro Ile Asp Pro Cys Arg Ala Gly Asn Gly Gly Cys His Gly
229     565               570               575
231 ctg gag ctg gag gca aat gcc cac ttc tcc atc ttc tac caa tgg ctt    1954
232 Leu Glu Leu Glu Ala Asn Ala His Phe Ser Ile Phe Tyr Gln Trp Leu
233 580               585               590               595
235 aag agt gcc ggc atc acg ctt cct gcc gac cgc cga gtc aca gcc ctg    2002
236 Lys Ser Ala Gly Ile Thr Leu Pro Ala Asp Arg Arg Val Thr Ala Leu
237               600               605               610
239 gtg ccc tcc gag gct gca gtc cgt cag ctg agc ccc gag gac cga gct    2050
240 Val Pro Ser Glu Ala Ala Val Arg Gln Leu Ser Pro Glu Asp Arg Ala
241               615               620               625
243 ttc tgg ctg cag cca agg acg ctg ccg aac ctg gtc agg gcc cat ttt    2098
244 Phe Trp Leu Gln Pro Arg Thr Leu Pro Asn Leu Val Arg Ala His Phe
245               630               635               640
247 ctc cag ggt gcc ctc ttc gag gag gag ctg gcc cgg ctg ggt ggg cag    2146
248 Leu Gln Gly Ala Leu Phe Glu Glu Glu Leu Ala Arg Leu Gly Gly Gln
249     645               650               655
251 gaa gtg gcc acc ctg aac ccc acc aca cgc tgg gag att cgc aac att    2194
252 Glu Val Ala Thr Leu Asn Pro Thr Thr Arg Trp Glu Ile Arg Asn Ile
253 660               665               670               675
255 agt ggg agg gtc tgg gtg cag aat gcc agc gtg gat gtg gct gac ctc    2242
256 Ser Gly Arg Val Trp Val Gln Asn Ala Ser Val Asp Val Ala Asp Leu
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257                   680            685                690
259 ctt gcc acc aac ggt gtc cta cac atc ctc agc cag gtc tta ctg ccc      2290
260 Leu Ala Thr Asn Gly Val Leu His Ile Leu Ser Gln Val Leu Leu Pro
261           695            700                705
263 ccc cga ggg gat gtg ccc ggt ggg cag ggg ttg ctg cag cag ctg gac      2338
264 Pro Arg Gly Asp Val Pro Gly Gly Gln Gly Leu Leu Gln Gln Leu Asp
265           710            715                720
267 ttg gtg cct gcc ttc agc ctc ttc cgg gaa ttg ctg cag cac cat ggg      2386
268 Leu Val Pro Ala Phe Ser Leu Phe Arg Glu Leu Leu Gln His His Gly
269      725            730                735
271 ttg gtg ccc cag att gag gct gcc act gcc tac acc atc ttt gtg ccc      2434
272 Leu Val Pro Gln Ile Glu Ala Ala Thr Ala Tyr Thr Ile Phe Val Pro
273 740            745                750                755
275 acc aac cgc tcc ctg gag gcc cag ggc aac agc agt cac ctg gac gca      2482
276 Thr Asn Arg Ser Leu Glu Ala Gln Gly Asn Ser Ser His Leu Asp Ala
277           760                765                770
279 gac aca gtg cgg cac cat gtg gtc ctg ggg gag gcc ctc tcc atg gaa      2530
280 Asp Thr Val Arg His His Val Val Leu Gly Glu Ala Leu Ser Met Glu
281           775                780                785
283 acc ctg cgg aag ggt gga cac cgc aac tcc ctc ctg ggc cct gcc cac      2578
284 Thr Leu Arg Lys Gly Gly His Arg Asn Ser Leu Leu Gly Pro Ala His
285           790            795                800
287 tgg atc gtc ttc tac aac cac agt ggc cag cct gag gtg aac cat gtg      2626
288 Trp Ile Val Phe Tyr Asn His Ser Gly Gln Pro Glu Val Asn His Val
289      805            810                815
291 cca ctg gaa ggc ccc atg ctg gag gcc cct ggc cgc tcg ctg att ggt      2674
292 Pro Leu Glu Gly Pro Met Leu Glu Ala Pro Gly Arg Ser Leu Ile Gly
293 820            825                830                835
295 ctg tcg ggg gtc ctg acg gtg ggc tca agt cgc tgc ctg cat agc cac      2722
296 Leu Ser Gly Val Leu Thr Val Gly Ser Ser Arg Cys Leu His Ser His
297           840                845                850
299 gct gag gcc ctg cgg gag aaa tgt gta aac tgc acc agg aga ttc cgc      2770
300 Ala Glu Ala Leu Arg Glu Lys Cys Val Asn Cys Thr Arg Arg Phe Arg
301           855            860                865
303 tgc act cag ggc ttc cag ctg cag gac aca ccc agg aag agc tgt gtc      2818
304 Cys Thr Gln Gly Phe Gln Leu Gln Asp Thr Pro Arg Lys Ser Cys Val
305           870                875                880
307 tac cga tct ggc ttc tcc ttc tcc cgg ggc tgc tct tac aca tgt gcc      2866
308 Tyr Arg Ser Gly Phe Ser Phe Ser Arg Gly Cys Ser Tyr Thr Cys Ala
309      885            890                895
311 aag aag atc cag gtg ccg gac tgc tgc cct ggt ttc ttt ggc acg ctg      2914
312 Lys Lys Ile Gln Val Pro Asp Cys Cys Pro Gly Phe Phe Gly Thr Leu
313 900            905                910                915
315 tgt gag cca tgc cca ggg ggt cta ggg ggg gtg tgc tca ggc cat ggg      2962
316 Cys Glu Pro Cys Pro Gly Gly Leu Gly Gly Val Cys Ser Gly His Gly
317           920                925                930
319 cag tgc cag gac agg ttc ctg ggc agc ggg gag tgc cac tgc cac gag      3010
320 Gln Cys Gln Asp Arg Phe Leu Gly Ser Gly Glu Cys His Cys His Glu
321           935                940                945
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gaagcatgca cagggaggag accantttta ttgcttgtct gggtggatgg ggcaggaggg 6723
nctgagggcc tgtcccagac aatannngtn ccctcgag   6761

location 6749

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RAW SEQUENCE LISTING ERROR SUMMARY        DATE: 08/14/2003
PATENT APPLICATION:  US/09/466,778A        TIME: 15:07:39

Input Set : A:\PF487 subst. SL Aug2003.txt
Output Set: N:\CRF4\08142003\I466778A.raw
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:1;  Xaa Pos. 2058,2109,2120,2122,2123
Seq#:2;  Xaa Pos. 2058,2109,2120,2122,2123
Seq#:4;  N Pos.  1103,1257,1290,1296,1298,1449,1485,1509,1510,1511,1514
Seq#:4;  Xaa Pos. 358,409,420,422,423
Seq#:5;  Xaa Pos. 358,409,420,422,423
Seq#:7;  N Pos.  36,51,248,508,521,564,933,945,951,958
Seq#:7;  Xaa Pos. 44,131,135,149,265,272,276,278,281
Seq#:8;  Xaa Pos. 44,131,135,149,265,272,276,278,281
Seq#:10; N Pos.  478,479,668,849,1138,1149,1157,1169,1172,1251
Seq#:10; Xaa Pos. 94,157,303,314,320,324,325,351
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Seq#:18; N Pos.  40
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Seq#:26; N Pos.  40
Seq#:28; N Pos.  21
Seq#:34; N Pos.  40
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